



BLAST Basic Local Alignment Search Tool

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BLASTN programs search nucleotide subjects using a nucleotide query. [more...](#)[Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number, gi, or FASTA sequence [?](#) [Clear](#)Query sequence(s) to be used for a BLAST search should be pasted in the text area. It automatically determines the format or the input. To allow this feature there are certain conventions required with regard to the input of identifiers. [more...](#)

NM_022162

Query subrange [?](#)From

To

Enter coordinates for a **subrange** of the query sequence. The BLAST search will apply only to the residues in the range. Sequence coordinates are from 1 to the sequence length. The range includes the residue at the **To** coordinate. [more...](#)

Or, upload file

 [Browse](#) [?](#)

Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.

Genetic code

 [?](#)

Job Title

NM_022162:Homo sapiens nucleotide-binding...

Enter a descriptive title for your BLAST search [?](#)

This title appears on all BLAST results and saved searches.

Align two or more sequences [?](#)

To get the CDS annotation in the output, use only the NCBI accession or gi number for either the query or subject. Reformat the results and check 'CDS feature' to display that annotation.

Enter Subject Sequence

Enter accession number, gi, or FASTA sequence [?](#) [Clear](#)

Subject sequence(s) to be used for a BLAST search should be pasted in the text area. It automatically determines the format of the input. To allow this feature there are certain conventions required with regard to the input of identifiers. [more...](#)

AC007728

Subject subrange [?](#)

From

To

Enter coordinates for a **subrange** of the subject sequence. The BLAST search will apply only to the residues in the range. Sequence coordinates are from 1 to the sequence length. The range includes the residue at the **To** coordinate. [more...](#)

Or, upload file



Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.

Choose Search Set

Database

Human genomic + transcript Mouse genomic + transcript Others (nr etc.):

Human genomic plus transcript (Human G+T)



Select the sequence database to run searches against. No BLAST database contains all the sequences at NCBI. BLAST databases are organized by informational content (nr, RefSeq, etc.) or by sequencing technique (WGS, EST, etc.). [more...](#)

Organism

Optional

Enter organism name or id - completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Select from the list or choose “Custom” to enter the name of an organism. The search will be restricted to the sequences in the database which are from the organism selected.

Entrez Query

Optional

Enter an Entrez query to limit search

You can use Entrez query syntax to search a subset of the selected BLAST database. This can be helpful to limit searches to molecule types, sequence lengths or to exclude organisms. [more...](#)

Program Selection

Optimize for

- Highly similar sequences (megablast)
- More dissimilar sequences (discontiguous megablast)
- Somewhat similar sequences (blastn)

Choose a BLAST algorithm

- Megablast is intended for comparing a query to closely related sequences and works best if the target percent identity is 95% or more but is very fast.
- Discontiguous megablast uses an initial seed that ignores some bases (allowing mismatches) and is intended for cross-species comparisons.
- BlastN is slow, but allows a word-size down to seven bases.

[more...](#)

Algorithm

- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)

Enter a PHI pattern [?](#)

Enter a PHI pattern to start the search. PHI-BLAST may perform better than simple pattern searching because it filters out false positives (pattern matches that are probably random and not indicative of homology).

Choose a BLAST algorithm [?](#)

- BlastP simply compares a protein query to a protein database.
- PSI-BLAST allows the user to build a PSSM (position-specific scoring matrix) using the results of the first BlastP run.)
- PHI-BLAST performs the search but limits alignments to those that match a pattern in the query.

BLAST

Search nucleotide sequence using Blastn (Optimize for somewhat similar sequences)

Show results in a new window

Algorithm parameters

General Parameters

Max target sequences

100 

Select the maximum number of aligned sequences to display [?](#)

Maximum number of aligned sequences to display (the actual number of alignments may be greater than this).

Short queries

Automatically adjust parameters for short input sequences [?](#)

Automatically adjust word size and other parameters to improve results for short queries.

Expect threshold

10 

Expected number of chance matches in a random model. [more...](#)

Word size

11

The length of the seed that initiates an alignment. [more...](#)

Scoring Parameters

Matrix

PAM30

Assigns a score for aligning pairs of residues, and determines overall alignment score. [more...](#)

Match/Mismatch Scores

2,-3

Reward and penalty for matching and mismatching bases. [more...](#)

Gap Costs

Existence: 5 Extension: 2

Cost to create and extend a gap in an alignment. Linear costs are available only with megablast and are determined by the match/mismatch scores. [more...](#)

Compositional adjustments

No adjustment

Matrix adjustment method to compensate for amino acid composition of sequences. [more...](#)

Filters and Masking

Filter

Low complexity regions

Mask regions of low compositional complexity that may cause spurious or misleading results. [more...](#)

Species-specific repeats for: Human

Mask repeat elements of the specified species that may lead to spurious or misleading results. [more...](#)

Mask

Mask for lookup table only

Mask query while producing seeds used to scan database, but not for extensions. [more...](#)

Mask lower case letters [\[?\]](#)

Mask any letters that were lower-case in the FASTA input. [more...](#)

Discontiguous Word Options

Template length

18

Total number of bases in a seed that ignores some positions. [more...](#)

Template type

Coding [\[?\]](#)

Specifies which bases are ignored in scanning the database. [more...](#)

PSI/PHI BLAST

PSSM

PSSM is uploaded... [Clear](#)

Upload PSSM Optional

Upload a Position Specific Score Matrix (PSSM) that you previously downloaded from a PSI-BLAST iteration. You may search a different database than that used to generate the PSSM, but you must use the same query. [more...](#)

PSI-BLAST Threshold

Set the statistical significance threshold to include a sequence in the model used by PSI-BLAST to create the PSSM on the next iteration.

BLAST

Search nucleotide sequence using Blastn (Optimize for somewhat similar sequences)

Show results in a new window

7 28 11 Linear Linear Linear Linear

Linear Existence: 5 Extension: 2

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Blast 2 sequences

NM_022162:Homo sapiens nucleotide-binding...

Results for: ref|NM_022162.1 Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA(4485bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|11545911|ref|NM_022162.1|

Description

Homo sapiens nucleotide-binding oligomerization domain containing 2 (NOD2), mRNA

Molecule type

rna

Query Length

4485

Subject ID

gi|14277249|gb|AC007728.4|AC007728

Description

Homo sapiens chromosome 16 clone RP11-327F22, complete sequence

Molecule type

nucleic acid

Subject Length

168271

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes

Filter string L;m;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

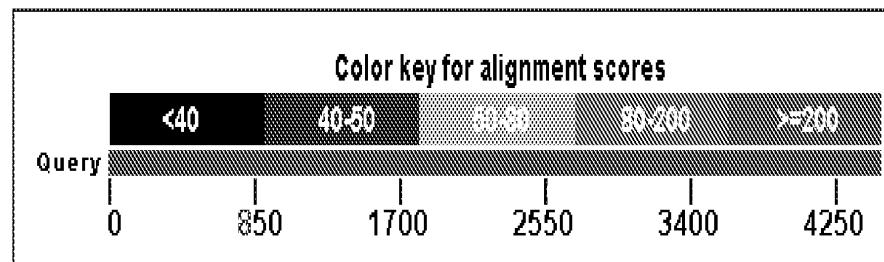
Effective search space 750722576

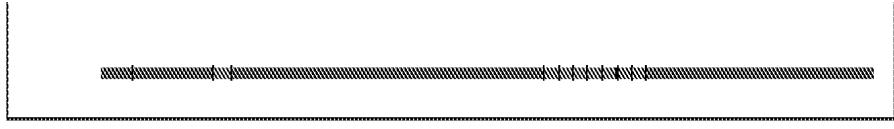
[Graphic Summary](#)

Distribution of 28 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.







Plot of gi|11545911|ref|NM_022162.1| vs gi|14277249|gb|AC007728.4|AC007728 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

AC007728.4	Homo sapiens chromosome 16 clone RP11-327F22, complete sequence	3279	8591	100%	0.0	100%
------------	---	------	------	------	-----	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree](#) of results

>gb|AC007728.4|AC007728 Homo sapiens chromosome 16 clone RP11-327F22, complete sequence
Length=168271

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 3279 bits (3636), Expect = 0.0
 Identities = 1818/1818 (100%), Gaps = 0/1818 (0%)
 Strand=Plus/Minus

Query 750	AGCTGCCACATGCAAGAAGTATATGCCAAGCTGAGGACCACGGTGTCTGCTCAGTCG	809
Sbjct 140450	AGCTGCCACATGCAAGAAGTATATGCCAAGCTGAGGACCACGGTGTCTGCTCAGTCG	140391
Query 810	CTTCCTCAGTACCTAATGATGGAGCAGAGACGCTCGCCTGGAGGGACATATAACAGAGAA	869
Sbjct 140390	CTTCCTCAGTACCTATGATGGAGCAGAGACGCTCGCCTGGAGGGACATATAACAGAGAA	140331
Query 870	TGTCCTGGAGGTCTGGCAGATGTGGCATGGCTGGACCCCCCAGAAGAGCCCAGCCAC	929
Sbjct 140330	TGTCCTGGAGGTCTGGCAGATGTGGCATGGCTGGACCCCCCAGAAGAGCCCAGCCAC	140271
Query 930	CCTGGGCCTGGAGGAGCTTCAGCACCCCTGGCACCTCAATGACGATGCGGACACTGT	989
Sbjct 140270	CCTGGGCCTGGAGGAGCTTCAGCACCCCTGGCACCTCAATGACGATGCGGACACTGT	140211
Query 990	GCTGGTGGTGGTGAGGCGGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCT	1049
Sbjct 140210	GCTGGTGGTGGTGAGGCGGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCT	140151
Query 1050	GTGGGCTGCAGGGCAAGACTTCAGGAATTCTCTTTGTCTTCCATTCAAGCTGCCGGCA	1109
Sbjct 140150	GTGGGCTGCAGGGCAAGACTTCAGGAATTCTCTTTGTCTTCCATTCAAGCTGCCGGCA	140091
Query 1110	GCTGCAGTGCATGGCAAACCACTCTGTGCGGACTCTACTCTTGAGCACTGCTGTTG	1169
Sbjct 140090	GCTGCAGTGCATGGCAAACCACTCTGTGCGGACTCTACTCTTGAGCACTGCTGTTG	140031
Query 1170	GCCTGATGTTGGTCAAGAAGACATCTCCAGTTACTCCTTGACCACCCCTGACCGTGTCT	1229
Sbjct 140030	GCCTGATGTTGGTCAAGAAGACATCTCCAGTTACTCCTTGACCACCCCTGACCGTGTCT	139971

Query	1230	GTTAACCTTGATGGCTTGACGAGTTCAAGTCAGGTTCACCGATCGTAAACGCCACTG 	1289
Sbjct	139970	GTTAACCTTGATGGCTTGACGAGTTCAAGTCAGGTTCACCGATCGTAAACGCCACTG 	139911
Query	1290	CTCCCCGACCGACCCACCTCTGTCCAGACCCCTGCTTCAACCTCTGCAGGGCAACCT 	1349
Sbjct	139910	CTCCCCGACCGACCCACCTCTGTCCAGACCCCTGCTTCAACCTCTGCAGGGCAACCT 	139851
Query	1350	GCTGAAGAATGCCCGCAAGGTGGTGACCAGCCGTCCGGCGCTGTGTCGGCTTCCTCAG 	1409
Sbjct	139850	GCTGAAGAATGCCCGCAAGGTGGTGACCAGCCGTCCGGCGCTGTGTCGGCTTCCTCAG 	139791
Query	1410	GAAGTACATCCGCACCGAGTTCAACCTCAAGGGTTCTCTGAACAGGGCATCGAGCTGTA 	1469
Sbjct	139790	GAAGTACATCCGCACCGAGTTCAACCTCAAGGGTTCTCTGAACAGGGCATCGAGCTGTA 	139731
Query	1470	CCTGAGGAAGCGCCATCATGAGCCGGGGTGGCGGACCGCCTCATCCGCCTGCTCCAAGA 	1529
Sbjct	139730	CCTGAGGAAGCGCCATCATGAGCCGGGGTGGCGGACCGCCTCATCCGCCTGCTCCAAGA 	139671
Query	1530	GACCTCAGCCCTGCACGGTTGTGCCACCTGCCGTCTCTCATGGATGGTGTCCAAATG 	1589
Sbjct	139670	GACCTCAGCCCTGCACGGTTGTGCCACCTGCCGTCTCTCATGGATGGTGTCCAAATG 	139611
Query	1590	CCACCAGGAACGTGTCAGGA TTGGGG TCCCCAAAGACCACTACAGATATGTACCT 	1649
Sbjct	139610	CCACCAGGAACGTGTCAGGA TTGGGG TCCCCAAAGACCACTACAGATATGTACCT 	139551
Query	1650	GCTGATTCTGCAGCATTTCTGCTGCATGCCA cccccc AGACTCAGCTTCCAAGGTCT 	1709
Sbjct	139550	GCTGATTCTGCAGCATTTCTGCTGCATGCCA cccccc AGACTCAGCTTCCAAGGTCT 	139491
Query	1710	GGGACCCAGTCTCTGGGGCCGCCTCCCCACCCCTCTGCACCTGGCAGACTGGCTCT 	1769
Sbjct	139490	GGGACCCAGTCTCTGGGGCCGCCTCCCCACCCCTCTGCACCTGGCAGACTGGCTCT 	139431
Query	1770	GTGGGGCCTGGCATGTGCTACGTGTTCTCAGCCCAGCAGCTCCAGGCAGCACAGGT 	1829
Sbjct	139430	GTGGGGCCTGGCATGTGCTACGTGTTCTCAGCCCAGCAGCTCCAGGCAGCACAGGT 	139371
Query	1830	CAGCCCTGATGACATTCTCTGGCTTCTGGTGGTGCCTGGGAG 	1889
Sbjct	139370	CAGCCCTGATGACATTCTCTGGCTTCTGGTGGTGCCTGGGAG 	139311
Query	1890	TACGGGCCCTGGAAATTCTCACATCACTTCCAGTGCTTCTTGCCTGCCTTACCT 	1949
Sbjct	139310	TACGGGCCCTGGAAATTCTCACATCACTTCCAGTGCTTCTTGCCTGCCTTACCT 	139251
Query	1950	GGCACTCAGTGATGTGCCACCAAGCTTGCTCAGACACCTCTCAATTGTGGCAGGCC 	2009
Sbjct	139250	GGCACTCAGTGATGTGCCACCAAGCTTGCTCAGACACCTCTCAATTGTGGCAGGCC 	139191
Query	2010	AGGCAACTCACCAATGCCAGGCTCTGCCACGATGTGCATCCAGGCCTGGAGGGAAA 	2069
Sbjct	139190	AGGCAACTCACCAATGCCAGGCTCTGCCACGATGTGCATCCAGGCCTGGAGGGAAA 	139131
Query	2070	GGACAGCAGCGTGGCAGCTTGCTGCAGAAGGCCAGCCGACAACCTTCAGATCACAGC 	2129
Sbjct	139130	GGACAGCAGCGTGGCAGCTTGCTGCAGAAGGCCAGCCGACAACCTTCAGATCACAGC 	139071
Query	2130	AGCCTTCTGGCAGGGCTGTTGTCCCGGGAGCACTGGGCCTGCTGGCTGAGTGCCAGAC 	2189

NCBI Blast:NM_022162:Homo sapiens nucleotide-binding...

Sbjct	139070	AGCCTTCCCTGGCAGGGCTGTTGCCGGAGCACTGGGCCTGCTGGCTGAGTGCCAGAC	139011
Query	2190	ATCTGAGAAGGCCCTGCTCCGGGCCAGGCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCT	2249
Sbjct	139010	ATCTGAGAAGGCCCTGCTCCGGGCCAGGCCTGTGCCCGCTGGTGTCTGGCCCGCAGCCT	138951
Query	2250	CCGCAAGCACTTCCACTCCATCCCAGTCGCACCGGGTGAGGCCAAGAGCGTGCATGC	2309
Sbjct	138950	CCGCAAGCACTTCCACTCCATCCCAGTCGCACCGGGTGAGGCCAAGAGCGTGCATGC	138891
Query	2310	CATGCCCGGTTCATCTGGCTCATCCGGAGCCTGTACGAGATGCAGGAGGAGCGGCTGGC	2369
Sbjct	138890	CATGCCCGGTTCATCTGGCTCATCCGGAGCCTGTACGAGATGCAGGAGGAGCGGCTGGC	138831
Query	2370	TGGAAAGGCTGCACGTGGCCTGAATGTTGGCACCTCAAGTTGACATTTCAGTGTGGG	2429
Sbjct	138830	TGGAAAGGCTGCACGTGGCCTGAATGTTGGCACCTCAAGTTGACATTTCAGTGTGGG	138771
Query	2430	CCCCACTGAGTGTGCTGCCCTGGCCTTGTGCTGCAGCACCTCCGGCGGCCGTGGCCCT	2489
Sbjct	138770	CCCCACTGAGTGTGCTGCCCTGGCCTTGTGCTGCAGCACCTCCGGCGGCCGTGGCCCT	138711
Query	2490	GCAGCTGGACTACAACCTGTGGGTGACATTGGCGTGGAGCAGCTGCTGCCTGCCTGG	2549
Sbjct	138710	GCAGCTGGACTACAACCTGTGGGTGACATTGGCGTGGAGCAGCTGCTGCCTGCCTGG	138651
Query	2550	TGTCTGCAAGGCTCTGTA 2567	
Sbjct	138650	TGTCTGCAAGGCTCTGTA 138633	

Score = 2401 bits (2662), Expect = 0.0

Identities = 1331/1331 (100%), Gaps = 0/1331 (0%)

Strand=Plus/Minus

Query	3155	GGCTCCGAGGAACACTTCTCTAGAGGAGGTGACAAGCTGGCTGCAGGGACACCA	3214
Sbjct	119260	GGCTCCGAGGAACACTTCTCTAGAGGAGGTGACAAGCTGGCTGCAGGGACACCA	119201
Query	3215	GACTCTGTTGAAGTCTCCGGAGGATGTTCGTCTCAGTTGTTGTGAGCAGGCTGT	3274
Sbjct	119200	GACTCTGTTGAAGTCTCCGGAGGATGTTCGTCTCAGTTGTTGTGAGCAGGCTGT	119141
Query	3275	GAGTTGGGCCAGAGGCTGGTGACATGTGTTGGCAGCCTCTCAAATGAGCCCTGT	3334
Sbjct	119140	GAGTTGGGCCAGAGGCTGGTGACATGTGTTGGCAGCCTCTCAAATGAGCCCTGT	119081
Query	3335	CCTGCCTAACGGCTGAACCTGTTCTGGAACACCATAGGTACCTTATTCTGGCAGAG	3394
Sbjct	119080	CCTGCCTAACGGCTGAACCTGTTCTGGAACACCATAGGTACCTTATTCTGGCAGAG	119021
Query	3395	GAGGGAGCATCAGTGCCTCCAGGATAGACTTTCCAAGCCTACTTTGCCATTGACTT	3454
Sbjct	119020	GAGGGAGCATCAGTGCCTCCAGGATAGACTTTCCAAGCCTACTTTGCCATTGACTT	118961
Query	3455	CTTCCCAAGATTCAATCCCAGGATGACAAGGACAGCCCTCTCCATAGTATGGACTG	3514
Sbjct	118960	CTTCCCAAGATTCAATCCCAGGATGACAAGGACAGCCCTCTCCATAGTATGGACTG	118901
Query	3515	GCCTCTGCTGATCCTCCCAGGCTCCGTGTGGTCAGTGGGCCATGGATGTGCTTGT	3574
Sbjct	118900	GCCTCTGCTGATCCTCCCAGGCTCCGTGTGGTCAGTGGGCCATGGATGTGCTTGT	118841

NCBI Blast:NM_022162:Homo sapiens nucleotide-binding...

Query	3575	AACTGAGTGCCTTTGGTGGAGAGGCCGGCCTCTCACAAAAGACCCCTTACCACTGCTC	3634
Sbjct	118840	AACTGAGTGCCTTTGGTGGAGAGGCCGGCCTCTCACAAAAGACCCCTTACCACTGCTC	118781
Query	3635	TGATGAAGAGGAGTACACAGAACACATAATTAGGAAGCAGCTTCCCCATGTCTCGACT	3694
Sbjct	118780	TGATGAAGAGGAGTACACAGAACACATAATTAGGAAGCAGCTTCCCCATGTCTCGACT	118721
Query	3695	CATCCATCCAGGCCATTCCCCGTCTGGTCCTCCCCCTCCCTGGACTCCTGCACACG	3754
Sbjct	118720	CATCCATCCAGGCCATTCCCCGTCTGGTCCTCCCCCTCCCTGGACTCCTGCACACG	118661
Query	3755	CTCCTTCCTCTGAGGCTGAAATTAGAACATATTAGTGACCTCAGCTTGTATTTCACTTA	3814
Sbjct	118660	CTCCTTCCTCTGAGGCTGAAATTAGAACATATTAGTGACCTCAGCTTGTATTTCACTTA	118601
Query	3815	CAGCACCCCCAACCTGGCACCCAGGGTGGGAAGGGTACACCTTAGCCTGCCCTCCTT	3874
Sbjct	118600	CAGCACCCCCAACCTGGCACCCAGGGTGGGAAGGGTACACCTTAGCCTGCCCTCCTT	118541
Query	3875	CCGGTGTAAAGACATTTGGAAGGGGACACGTGACAGCGTTGTTCCCCAAGACATT	3934
Sbjct	118540	CCGGTGTAAAGACATTTGGAAGGGGACACGTGACAGCGTTGTTCCCCAAGACATT	118481
Query	3935	CTAGGTTGCAAGAAAAATATGACCACACTCCAGCTGGGATCACATGTGGACTTTATTT	3994
Sbjct	118480	CTAGGTTGCAAGAAAAATATGACCACACTCCAGCTGGGATCACATGTGGACTTTATTT	118421
Query	3995	CCAGTGAAATCAGTTACTCTCAGTTAACGCTTGGAAACAGCTCGACTTTAAAAGCTC	4054
Sbjct	118420	CCAGTGAAATCAGTTACTCTCAGTTAACGCTTGGAAACAGCTCGACTTTAAAAGCTC	118361
Query	4055	CAAATGCAGCTTAAAAATTAAATCTGGGCCAGAATTCAAACGGCCTCACTAGGCTTCT	4114
Sbjct	118360	CAAATGCAGCTTAAAAATTAAATCTGGGCCAGAATTCAAACGGCCTCACTAGGCTTCT	118301
Query	4115	GGTTGATGCCTGTGAACACTGACAACAGACTCTGAAATAGACCCACAAGAGGCA	4174
Sbjct	118300	GGTTGATGCCTGTGAACACTGACAACAGACTCTGAAATAGACCCACAAGAGGCA	118241
Query	4175	GTTCCATTCAATTGTGCCAGAATGCTTCTGGATGTACAGTTATGGATTGAAAGTTACA	4234
Sbjct	118240	GTTCCATTCAATTGTGCCAGAATGCTTCTGGATGTACAGTTATGGATTGAAAGTTACA	118181
Query	4235	GGaaaaaaaaATTAGGCCGTTCTCAAAGCAAATGTCTCTGGATTATTCAAATGATG	4294
Sbjct	118180	GGaaaaaaaaATTAGGCCGTTCTCAAAGCAAATGTCTCTGGATTATTCAAATGATG	118121
Query	4295	TATGTTGAAGCCTTGTAAATTGTCAAGATGCTGTGCAAATGTTATTATTTAACATTAT	4354
Sbjct	118120	TATGTTGAAGCCTTGTAAATTGTCAAGATGCTGTGCAAATGTTATTATTTAACATTAT	118061
Query	4355	GATGTGTGAAACTGGTTAATATTATAGGTCACTTGTCTTACTGTCTTAAGTTATAC	4414
Sbjct	118060	GATGTGTGAAACTGGTTAATATTATAGGTCACTTGTCTTACTGTCTTAAGTTATAC	118001
Query	4415	TCTTATAGACAACATGGCCGTGAACCTTATGCTGTAAATAATCAGAGGGAAATAACTGT	4474
Sbjct	118000	TCTTATAGACAACATGGCCGTGAACCTTATGCTGTAAATAATCAGAGGGAAATAACTGT	117941
Query	4475	TGAGTCAAAAC 4485	
Sbjct	117940	TGAGTCAAAAC 117930	

Score = 848 bits (940), Expect = 0.0
 Identities = 473/475 (99%), Gaps = 0/475 (0%)
 Strand=Plus/Minus

Query	172	TCTCCGGTTGTGAAAITGCTCGCAGGAGGCTTCAGGCACAGAGGAGCCAGCTGGTC	231
Sbjct	151525	TCCCCAGGTGTGAAATGCTCGCAGGAGGCTTCAGGCACAGAGGAGCCAGCTGGTC	151466
Query	232	GAGCTGCTGGTCTCAGGGTCCCTGGAAGGCTTCAGAGAGTGTCTGGACTGGCTGTGTC	291
Sbjct	151465	GAGCTGCTGGTCTCAGGGTCCCTGGAAGGCTTCAGAGAGTGTCTGGACTGGCTGTGTC	151406
Query	292	TGGGAGGTCTCTCCTGGAGGACTACGAGGGCTCCACCTCCTGGGCCAGCCTCTCC	351
Sbjct	151405	TGGGAGGTCTCTCCTGGAGGACTACGAGGGCTCCACCTCCTGGGCCAGCCTCTCC	151346
Query	352	CACTTGCCAGGCCTCTGGACACCGTCTGGATAAGGGTACTGGGCCTGTCAGAAG	411
Sbjct	151345	CACTTGCCAGGCCTCTGGACACCGTCTGGATAAGGGTACTGGGCCTGTCAGAAG	151286
Query	412	CTCATCGCGCTGCCAAGAAGCCAGGCCAGGCCAGTCCCCAAGCTGCATGGCTGC	471
Sbjct	151285	CTCATCGCGCTGCCAAGAAGCCAGGCCAGGCCAGTCCCCAAGCTGCATGGCTGC	151226
Query	472	TGGGACCCCCACTCGCTCCACCCAGCCCAGACCTGCAGAGTCACCGGCCAGCCATTGTC	531
Sbjct	151225	TGGGACCCCCACTCGCTCCACCCAGCCCAGACCTGCAGAGTCACCGGCCAGCCATTGTC	151166
Query	532	AGGAGGCCTCACAGCCATGTGGAGAACATGCTGGACCTGGCATGGAGCGGGGTTCGTC	591
Sbjct	151165	AGGAGGCCTCACAGCCATGTGGAGAACATGCTGGACCTGGCATGGAGCGGGGTTCGTC	151106
Query	592	AGCCAGTATGAATGTGATGAAATCAGGTGCCGATCTCACACCGTCCCAGAGGG	646
Sbjct	151105	AGCCAGTATGAATGTGATGAAATCAGGTGCCGATCTCACACCGTCCCAGAGGG	151051

Score = 325 bits (360), Expect = 6e-90
 Identities = 180/180 (100%), Gaps = 0/180 (0%)
 Strand=Plus/Minus

Query	1	GTAGACAGATCCAGGCTACCAGTCCTGTGCCACTGGCTTTGGCGTCTGCACAAGGC	60
Sbjct	153867	GTAGACAGATCCAGGCTACCAGTCCTGTGCCACTGGCTTTGGCGTCTGCACAAGGC	153808
Query	61	CTACCCGCAGATGCCATGCCCTGCTCCCCAGCCTAATGGGCTTGATGGGGAAAGAGGGT	120
Sbjct	153807	CTACCCGCAGATGCCATGCCCTGCTCCCCAGCCTAATGGGCTTGATGGGGAAAGAGGGT	153748
Query	121	GGTCAGCCTCTCACGATGAGGAGGAAAGAGCAAGTGTCTCTCGGACATTCTCGGGT	180
Sbjct	153747	GGTCAGCCTCTCACGATGAGGAGGAAAGAGCAAGTGTCTCTCGGACATTCTCGGGT	153688

Score = 194 bits (214), Expect = 3e-50
 Identities = 107/107 (100%), Gaps = 0/107 (0%)
 Strand=Plus/Minus

Query	645	GGCAAGAAGGCTGTTGATCTGCCACGGTGAAAGCGAATGGATTGGCTGCCTCCTCT	704
Sbjct	143152	GGCAAGAAGGCTGTTGATCTGCCACGGTGAAAGCGAATGGATTGGCTGCCTCCTCT	143093

Query 705 ACAACATGTTCAGGAATTACCAGTCCCATTGGCCCTGCCTTGGAAAG 751
 Sbjct 143092 ACAACATGTTCAGGAATTACCAGTCCCATTGGCCCTGCCTTGGAAAG 143046

Score = 158 bits (174), Expect = 2e-39
 Identities = 87/87 (100%), Gaps = 0/87 (0%)
 Strand=Plus/Minus

Query 2987 GCCTGGAGGAGAACCACTCCAGGTGAAGGTGTATGTTCTCTCGCAGAAGGACTGAAGA 3046
 Sbjct 125518 GCCTGGAGGAGAACCACTCCAGGTGAAGGTGTATGTTCTCTCGCAGAAGGACTGAAGA 125459

Query 3047 AAAATTCAAGTTGAAAATCCTGAAGT 3073
 Sbjct 125458 AAAATTCAAGTTGAAAATCCTGAAGT 125432

Score = 158 bits (174), Expect = 2e-39
 Identities = 87/87 (100%), Gaps = 0/87 (0%)
 Strand=Plus/Minus

Query 2901 CAGCCTGGTGGGGAAACACATTGGCAGTGTGGGTGCCAAGCCTGGCACTGATGCTGGC 2960
 Sbjct 127708 CAGCCTGGTGGGGAAACACATTGGCAGTGTGGGTGCCAAGCCTGGCACTGATGCTGGC 127649

Query 2961 AAAGAACGTCATGCTAGAAGAACTCTG 2987
 Sbjct 127648 AAAGAACGTCATGCTAGAAGAACTCTG 127622

Score = 156 bits (172), Expect = 6e-39
 Identities = 86/86 (100%), Gaps = 0/86 (0%)
 Strand=Plus/Minus

Query 2734 AGGCTGGGAATAACTACATCACTGCCGCGGGAGGCCAAGTGCTGGCGAGGGGCTCCGA 2793
 Sbjct 131083 AGGCTGGGAATAACTACATCACTGCCGCGGGAGGCCAAGTGCTGGCGAGGGGCTCCGA 131024

Query 2794 GGCAACACCTCCTGCAGTTCTGGG 2819
 Sbjct 131023 GGCAACACCTCCTGCAGTTCTGGG 130998

Score = 154 bits (170), Expect = 2e-38
 Identities = 85/85 (100%), Gaps = 0/85 (0%)
 Strand=Plus/Minus

Query 3072 GTTGTCCAATAACTGCATCACCTACCTAGGGCAGAAGCCCTCTGCAGGCCCTGAAAG 3131
 Sbjct 121188 GTTGTCCAATAACTGCATCACCTACCTAGGGCAGAAGCCCTCTGCAGGCCCTGAAAG 121129

Query 3132 GAATGACACCACCATCCTGGAAAGTCTGG 3156
 Sbjct 121128 GAATGACACCACCATCCTGGAAAGTCTGG 121104

Score = 154 bits (170), Expect = 2e-38
 Identities = 85/85 (100%), Gaps = 0/85 (0%)
 Strand=Plus/Minus

Query 2819 GATTCTGGGGCAACAGAGTGGGTGACGAGGGGGCCAGGCCCTGGCTGAAGCCTGGGTG 2878

```

Sbjct 128385 |||||||GATTCTGGGCCAACAGACTGGGTGACGAGGGGGCCCAGGCCCTGGCTGAAGCCTGGTG 128326
Query 2879 ATCACCAAGAGCTTGAGGTGGCTCAG 2903
Sbjct 128325 |||||||ATCACCAAGAGCTTGAGGTGGCTCAG 128301

```

Score = 154 bits (170), Expect = 2e-38
 Identities = 85/85 (100%), Gaps = 0/85 (0%)
 Strand=Plus/Minus

```

Query 2652 TCTATTCAACAACAAATTGACTGACGGCTGTGCACACTCCATGGCTAAGCTCCTTGCATG 2711
Sbjct 134115 |||||||TCTATTCAACAACAAATTGACTGACGGCTGTGCACACTCCATGGCTAAGCTCCTTGCATG 134056
Query 2712 CAGGCAGAACTTCTTGGCATTGAGG 2736
Sbjct 134055 |||||||CAGGCAGAACTTCTTGGCATTGAGG 134031

```

Score = 154 bits (170), Expect = 2e-38
 Identities = 90/92 (97%), Gaps = 1/92 (1%)
 Strand=Plus/Minus

```

Query 2561 CTCTGTA-TTGCGCGATAACAATATCTCAGACCGAGGCATCTGCAAGCTCATTGAATGT 2619
Sbjct 134427 |||||||CTCTTAGTTGCGCGATAACAATATCTCAGACCGAGGCATCTGCAAGCTCATTGAATGT 134368
Query 2620 GCTCTTCACTGCGAGCAATTGAGAAGTTAGC 2651
Sbjct 134367 |||||||GCTCTTCACTGCGAGCAATTGAGAAGTTAGC 134336

```

Score = 35.6 bits (38), Expect = 0.015
 Identities = 22/24 (91%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

```

Query 4221 ATTGAAAGTTTACAGGaaaaaaa 4244
Sbjct 60530 |||||||ATTAACAGTTTACAGGAAAAAAA 60553

```

Score = 30.1 bits (32), Expect = 0.63
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Plus

```

Query 281 GGCTGCTGTCCTGGGAGGT 299
Sbjct 131339 |||||||GGCAGCTGTCCTGGGAGGT 131357

```

Score = 30.1 bits (32), Expect = 0.63
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```

Query 339 CCAGCCTCTCTCCCAC TTG 357
Sbjct 136285 |||||||CCTGCCTCTCTCCCAC TTG 136267

```

Score = 30.1 bits (32), Expect = 0.63
 Identities = 16/16 (100%), Gaps = 0/16 (0%)

NCBI Blast:NM_022162:Homo sapiens nucleotide-binding..

Strand=Plus/Plus

Query	1098	CAGCTGCCGGCAGCTG	1113
Sbjct	140087	CAGCTGCCGGCAGCTG	140102

Score = 28.3 bits (30), Expect = 2.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query	2801	CCTCCTTGCAGTTCC	2815
Sbjct	8417	CCTCCTTGCAGTTCC	8403

Score = 28.3 bits (30), Expect = 2.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query	953	GCACCCCTGGCCACC	967
Sbjct	109718	GCACCCCTGGCCACC	109732

Score = 28.3 bits (30), Expect = 2.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Plus

Query	2283	ACCGGGTGAGGCCAAGAGCGTGCAT	2307
Sbjct	160465	ACAGGCTGAGTGCAAGAGCGTGCAT	160489

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query	1064	AAGACTTCCAGGAA	1077
Sbjct	1485	AAGACTTCCAGGAA	1472

Score = 26.5 bits (28), Expect = 7.7
Identities = 26/34 (76%), Gaps = 0/34 (0%)
Strand=Plus/Minus

Query	1608	GCAGGGAGGTCTGTCCCTAAACCCACTACAGAT	1641
Sbjct	10423		1039

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query	3051	TTCAGTTGAAAA	3064
Sbjct	68988	TTCAGTTGAAAA	69001

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)

Strand=Plus/Plus

Query 4154 GAAATAGACCCACA 4167

Sheet 70121 GAAATAGACGGCA 70124

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 3807 TTCACTTACAGCAC 3820

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 2983 CTCTGCCTGGAGGA 2996

Sbjct 140359 CTCTCCCTCCACCA 140346

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 3015 AGGTGTATGTTCTC 3028

Score = 26.5 bits (28), Expect = 7.7
Identities = 17/19 (89%), Gaps = 0/19 (0%)
Strand-Plus/Minus

Query	4060	GCAGCTTAAAAATTAAAT	4078
Sbjct	160764	GCATCTTAAAAATAAAT	160746

Score = 26.5 bits (28), Expect = 7.7
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 3015 AGGTGTATGTTCTC 3028

Start: 164007 1GCTGTATCTTC 165010

Subjct 16499 / AGGIGIAIGIICIC 165010

Select All Get selected sequences Distance tree of results